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Metagenomics: Novel Approach to Access Genetic Diversity

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Metagenomics is the study of genomes derived from environmental samples which circumvent conventional culture-based method. Metagenomic approaches provide a new insight into the bacterial diversity. Through this approach, enormous amounts of yet-to-be discovered bacterial diversity can be revealed. This culture-independent method has also greatly accelerated the pace of discovery of novel genes from the uncultured community. However, recovery of soil metagenomic DNA has become the major challenge. Soil metagenomic DNA is often co-purified with polyphenolic compounds and contaminants which will interfere with the downstream applications. Here we demonstrated a DNA extraction method which coupled with enzymatic and chemical lysis that enabled the recovery of HMW DNA from forest topsoil. The DNA recovered was of high quality and high purity, retained DNA size ranged up to 290 kb. The DNA could be subjected to PCR amplification and metagenomics library construction without the need of further purification steps. Sequence analysis revealed that microbial community in the Rimba Ilmu soil metagenome was affliated with members of phyla *acidobacteria, proteobacteria, actinobacteria, gemmatimonadetes, Candidate division TM6*, basidiomycota, ascomycota and planctomycetes. This indicated that this DNA extraction method had successfully recovered a wide range of microorganisms including the Gram-positive bacteria and fungi.